

Figure 1A

1	CGGACCGCGTGGGGGCGCGAGCCCTGGCTGACCTGATCCTGGACTAGTGGCCCGACCGCGGGG	60
61	CGCCCGGTGCGCGAGATGCTGGCCCGAGCCGAGCGGCTGCTCTTCACTCTGSAACGGCGCGG	120
1	M L A Q P Q R L L F I L D G A D	16
121	ACGAGCTGCGCGCGCTGGGGGGGCGCGGAGCGCGCGGCGCTGACAGACCCCTTCGAGCGCGG	180
17	E L P A L G G P E A A P C T D P F E A A	36
181	CGAGCGGCGCGCGCTGCTAGGCGCGGCTGCTGAGTAAAGCGCTGCTGGCCCGCGGCGCTCC	240
37	S G A E V L G E L L S K A L L P T A L L	56
241	TGCTGGTGACCAAGCGCGCGCGCGCGCGCGGAGGCTGCAAGCGCGCGCTGCTTCCCGG	300
57	L V T T R A A A P S R L Q G R L C S P Q	76
361	ATGCGCGCGAGCTGCGCGCGCTTCCTCGACAAGACAAAGAAAGATATTTCTACAAAGTTCT	360
77	C A E V R G F S D K D K K K Y F Y K F F	96
361	TCCGGGATGAGAGGAGGGCGGAGCGCGCTACCGCTTCTGAGGAGAAACGAGAGCTGT	420
97	R D E R R A E R A Y R F V K E N E T L E	116
421	TGCGCTGTGCTTCTGCGCCTTCTGTGCTGGATCTGTGCAACCTGCTGCGCGAGCAGC	480
117	A L C F N E E V C W V T V L R Q Q L	136
481	TGGAGCTCGGTGCGGACCTGTGCGCGCAGCTCAAGACCACCAAGCAGGTAGCTGCTTT	540
137	E L G F D L S F T S H T T T S V Y L L E	156
541	TCATCACCAGCGTTCTGAGCTCGGCTCGGCTAGCCGACCGGCGCGCGGTTGCAGGGCGACC	600
157	I T S V L S S A P V A D G P R L Q G D L	176
601	TGCGCAATCTGTGCGCGCTGGCCCGCGAGGGGCTCCTCGGAGCGAGGGCGCAGTTTGCGG	660
177	R N L C E L A F E G V L G R R A Q F A E	196
661	AGAAGGAAGTGCAGCAACTGGAGCTTCTGCGCTCCAAAGTGCAGACGCTGTTTCTCAGCA	720
197	K E L E Q L E L R G D K V Q T L F L S K	216
721	AAAAGGAGTGLCGGCGTCTGAGACAGAGTCACTACCGAGTTGATCCACCAGAGCT	780
217	K E L P G V L E T E V T Y Q F I D Q S F	236
781	TCCAGGAGTTCTCGCGGCACTGTCTACCTGCTGGAGGACGGCGGGGTGCCACGACCG	840
237	Q E F L A A L S Y L L E I G G V P R T A	256
841	CGAGGCGAGTGGAGAGCTCTGCTGGGAGGCGGAGCGGAGAGCACTGCTGCT	900
257	A G G V G T L L P G D A Q P H S H L V I	276

Figure 1B

901	TCACCACGCGCTTCTCTTTCCGACTGCTGAGCGCGGAGCGGATGCGCGACATCGAGCGCC	960
977	T T R F L F G L L S A E R M E D I E R H	296
1061	ACTTCGGCTGCATGCTTTTCAGAGCGCTGTGAAGCAGGAGCGCCCTGCGGTGGGTGCAGGGAC	1020
1097	F G C M V S E R V K Q E A L E W V Q G Q	316
1121	AGGGACAGGGCTGCTCCCGAGTGGCACCAGAGGTGACCCAGGGGGCCAAAGGGCTCCAGG	1080
117	G Q Q Q P G V A P E V T E G A K G L E D	336
1181	ACACCGAAGAGGCCAGGAGGAGGAGGAGGAGGAGGCCAACTACCCACTGGAGITGC	1140
1337	T R E P E E E E E G E E P N Y P L E L L	356
1141	TGTACTGCTGTGTACGAGAGCGAGGAGGAGCGGTTTGTGCGCCAAAGCCCTGTGCGGTTCC	1200
1357	Y Q L Y E T Q E D A F V R Q A L C R F P	376
1201	CGGAGCTGCGGCTGTAGCGAGTGGGCTTCTGCGCATGACGTGCGCTGTTCTGAGCTACT	1260
1377	E L A L Q R V R F C R M D V A V L S Y Q	396
1261	GCGTGAGGTGCTGCGCTCTGTGAGGAGCACTGCGGCTGATCAGCTGCAGATTGCTTCTG	1320
1397	V R C C P A G Q A L R L I S C R L V A A	416
1321	CGCAGGAGAGAGAGAGAGAGAGCGCTGGGGAGGCGGCTCCAGGCCAGGCTGGGTGCGCGCA	1380
1417	Q E K K K K S L G A R L Q A C L G G S S	436
1381	GTTCTCAAGSCACACAAACAACTGCCAGGCTCCCTTCTTCATCCACTCTTTCCAGGCA	1440
1437	S Q G T T K Q L P A S L L H P L F Q A M	456
1441	TGACTGACCCACTGTGGCATCTGAGCAGGCTCACGCTGTCCCACTGCCAACTGCGCTGACG	1500
1457	T D P L L H L S S L T L S H C K L P D A	476
1501	CGGTCTGCGGAGACCTTTCTGAGGCCCTGAGGGCAGCCTCCCGCACTGACGGAGCTGGGGC	1560
1477	V C R D L S E A L R A A P A L T E L G L	496
1561	TCTTCCACAACAGGCTCAGTGAGGCGGGACTGCGTATGCTGAGTGAGGGCTAGCTTGGC	1620
1497	L H N R L S E A G L R M L S E G L A W P	516
1621	CGCAGTGACGGGTGCAGACGGTTCAGGTACAGCTGCTGACCCCCAGCGAGGCTCCAGT	1680
1617	Q C R V Q T V R V Q L P D P Q R G L Q Y	536
1681	ACCTGGTGGGTATGCTTCGGCAGAGCCCGGCCCTGACCACCCTGGATCTCAGCGGCTGCC	1740
1537	L V G M L R Q S P A L T T L P L S G C Q	556
1741	AACTTCTCCCGCATGCTTACCTTCTGTCTGAGTCTGTGAATAAGGATCTGGCC	1800
1557	L E A F M V T Y L C A V L Q E Q G C G L	576

Figure 1C

[illegible]

Figure 2A

	1	50
HLERS11	(1)	-----
caspase_recruitment_protein	(1)	MAGGAWGR LA CTLE FF KFE FI EP QL LANKAHSRSSSSGETPA CF ERTS C
crycopyrin	(1)	-MASTRCK LA RYLE DD EDVD LI FI MM EDYP Q KGCIP LR GTSP AF CH
Nucleotide_Binding_Site	(1)	----MGFN QA LE EQ SQ DE LS FR Y IT TFSS AE LQ KI PK EV DL AG C
	51	100
HLERS11	(1)	-----
caspase_recruitment_protein	(51)	MEVAST VA QY GE RAW DL AHTW EL GL RS LCAC AE GAGHS FF PFYS F
crycopyrin	(50)	VD LA TLMIDFN GE KAW AM AVWI SA IN ER DI YK LR DE PF WG SDNA EN
Nucleotide_Binding_Site	(47)	KQ IV EI IT THCDSY W EMAS QV E ER K ER MDLS ER AP DE VFEA AL KS FN H
	101	150
HLERS11	(1)	-----
caspase_recruitment_protein	(101)	SEPHLGSPSQFTSTAVLMPWIHELPA GC TQGSERRV LE QL ED TSGERW EE
crycopyrin	(100)	SN-----
Nucleotide_Binding_Site	(97)	RK-----
	151	200
HLERS11	(1)	-----
caspase_recruitment_protein	(151)	LSASHLYQALPSSPDHESPSQESFNAPTSTAVLG SW GSPPC PS LAF FE Q OR
crycopyrin	(102)	-----STVIC Q Q DS
Nucleotide_Binding_Site	(99)	-----PLSLG IT R-----
	201	250
HLERS11	(1)	-----
caspase_recruitment_protein	(201)	APGTQW LE ETSGI YY PI ER ERER ES EKGRPPWAAVVGTH EQ AHSS LP
crycopyrin	(111)	TE EW ME LE Y SS ISICKMK Y Y RY K RY VRS RF Q IE LRN RL GES V
Nucleotide_Binding_Site	(107)	ER PP LDV EN ER FE FE EA QD EN CR IL KT KE EMAK SW SGDS FE V Q V
	251	300
HLERS11	(1)	-----
caspase_recruitment_protein	(211)	HHHPWEP VR ELCSTW FW EN DF NQ FT QLLL Q RP NR PSQD PL VER RS W
crycopyrin	(111)	HLNKRY TL EL LI LE HE HSQ Q ER DE LLA IG ET FT CS EV -----
Nucleotide_Binding_Site	(157)	MA RY RM LI PF SN PR-----
	301	350
HLERS11	(1)	-----
caspase_recruitment_protein	(301)	PDYVEEN GH LE IR DL FG PG DT Q EB RI VI LOGA AG IGH ST LA RV KEA
crycopyrin	(199)	-----SPIKMELL FD PD DE HSE PV HT VF GA AG IGH IL ARM ML D
Nucleotide_Binding_Site	(172)	-----V PG PFSY DV V Y EP AG LGH TT LA CH L LD
	351	400
HLERS11	(1)	-----M GA
caspase_recruitment_protein	(351)	WGR GO Y GC PR Q HV EN FS CR EAQSKV VS LA ET IG K GTAT PA P FC LS
crycopyrin	(241)	WAS GT LC CP PS GL FI IH FE VS LV TQ RS GD MS CC ED NP CH K IV E
Nucleotide_Binding_Site	(202)	WAEDN IK H S AA YL SC PE SS RL GP CS FE ED V FR WE EL QDD FE LA
	401	450
HLERS11	(4)	Q ER L FL LG AE EP FA GG EA AP CT EP FE AS CA RV GG SS AA LP
caspase_recruitment_protein	(401)	R ER L FL RG VE EP SW VE SS EL CH MS Q PC AD AL GS GH IT LE
crycopyrin	(291)	R SR I EL MG GP EC Q CF DE H GP CT DR Q ER SC II SS IF K IL P
Nucleotide_Binding_Site	(251)	Q AK I EV IG FE EL GA PG AL ED IC GE WE K EV VP VL GS IN FM LS
	451	500
HLERS11	(53)	T AL LV TA AA PG R GR CS QA ET RG FS DK K K K FE FE ER R
caspase_recruitment_protein	(451)	EAS FI IA RT TE QN IPS QA RW EL GG FS SS RR EN FR ST EP CA
crycopyrin	(241)	EAS LI IT FE VE LE K CH LD HE RH VE IG FS EAK RE FF FK ES EA Q
Nucleotide_Binding_Site	(301)	FA AL V TF FE RD RI AE E I YIR EC LE ED K RA SL RH SG ED CA
	501	550
HLERS11	(103)	BRAY FR EN ET EL AL CE VF Y Q W EN CV LR Q LE L GR LS RT ST FT SV
caspase_recruitment_protein	(501)	IRAF RV SN KE L WA GL FW SL LA CT GL M Q KK RE K IT L ST TT TL
crycopyrin	(391)	HA AS LI Q ENE VL ET MC IF LN Q W IV CT GL Q Q ES CK SL AC ST TT AV
Nucleotide_Binding_Site	(411)	MR AF EM RS NA AL FL LS AP AW CV IV CT TL L QL ME K GE EP VP FC IT FG L
	551	600
HLERS11	(157)	YL SI TS VL SS AE VAD EN PL Q EL RL NE GL RA FG VL GR AA EA KE LE QL
caspase_recruitment_protein	(551)	LY LA QA LA CA FE -----L GP QL RL CL SL AA EG IV Q K EL ES FD LR KH
crycopyrin	(441)	YV FL SL LP PG GS CH GL LA HL NG LC SLA AD GI WN Q N LF ES DL R NH
Nucleotide_Binding_Site	(411)	PL EL CS RF FE ---- Q CA L FE LE FT SL LA Q GL WA CT SV LR ED LE RL

Figure 2B

		501		650
HLRPS11	(202)	EIRGSKVQLFLSKKE	PGVLETVTYQFI	DQSFQEFLLAALSYLLEGGV
caspase_recruitment_protein	(591)	GIDGAIITSTFKK--	ILQHPHPLSY	SFIHLCEQEFFAAMSYVLEDEI-
crispypyrin	(491)	GLCKADYSATFRN	LFCKEVDCK	KFYSPFIHMTFQEFFAAMYKLEEEKE
Nucleotide_Binding_site	(440)	GVGESDLRLFLDGS	IFEDRVSKGCS	YSFIHLSFQCLTLFLVYTLKKEE
		651		700
HLRPS11	(153)	PTTAAGC	-----VGTLL	EGDAQPHSHLVLTTRFLEGLLSAEFRMD
caspase_recruitment_protein	(641)	-----	SGGFHSNQLID	LKRTLEAYGINGLFGASTTRFLLSLSDDEGERE
crispypyrin	(540)	GRTNVFCSFLKLP	SDVTVLEEN	YGKFEKGYLIFVVRFLLGLVNCERTSY
Nucleotide_Binding_site	(491)	EDRDGHTWIG	----DVCKL	SGVERLRNPDLIQAGYYSFGLANEKRAKE
		701		750
HLRPS11	(193)	IERHFGCMVSEEV	YCEALPFWQGG	QGCCPGVAPEVTEGAFLEDTEEERE
caspase_recruitment_protein	(681)	MEMLFHCLSS	---GRNLMQVPS	-----QLLLQPHS-----
crispypyrin	(150)	LEKKLSCKISQ	LRLELKKIEVF	-----ARAKKLQIQEES
Nucleotide_Binding_site	(641)	LEATFGCRMSEP	KQELLKCDIS	-----KCGSTVFLKQ
		751		800
HLRPS11	(243)	EEEGEETNYF	LELLYCLYETQ	EDAFVRCALCRFPELALQVRVPCFMDVAV
caspase_recruitment_protein	(710)	-----	LESILHCLYET	RNKKVLTQVMHFFEMGMC--VETDMELLV
crispypyrin	(670)	-----	LELFYCLYEM	QEEDEVQRADLYFKIEIN--LSTRMDHNV
Nucleotide_Binding_site	(670)	-----	ELLGOLYES	QEEBELWKEVMAOFFSTSLH--LNAVDEVVP
		801		850
HLRPS11	(293)	LSYCVPR	CHAGAPPLIS	RLVAACERKKKSLGRRLQASLGGSQ---
caspase_recruitment_protein	(714)	CWECIEPSHHK	LQLLEFQHEST	WTFEMVVIPEWVPVTAAYWQLLS-
crispypyrin	(694)	SSFCIECHHVES	LSLGLHNMFK	EEEEEEHGRHDMVQVLPSSSHAA
Nucleotide_Binding_site	(610)	SSFCVHCHNLQ	MSIQVIKENL	PENVVTASESDAEVRSQDQHMPEFWT
		851		900
HLRPS11	(343)	-----	-----	-----
caspase_recruitment_protein	(810)	-----	-----	-----
crispypyrin	(714)	CSHGLVMSH	-----	-----LT
Nucleotide_Binding_site	(660)	DLCSEFMSN	ELMGLAINDS	FLSASLVFLLCEQIASDTCHLQFVVEKNIS
		901		950
HLRPS11	(393)	-----	-----GTTK	QLFASLLHPLQAMTDECHSSLET
caspase_recruitment_protein	(860)	-----	VLKVTENL	LELDLSNSLSHSAVKSCKTLREHCHETLR
crispypyrin	(725)	SSFCRGLES	VLSTSQS	TELDLSNSLSGPMRVLCETLOEHCNIRLW
Nucleotide_Binding_site	(610)	PADAHENCL	LALEGHKT	VTYLTLLGNICDMFEALCEVLRHFFCNRTYLG
		951		1000
HLRPS11	(443)	LSHCKEPDAV	CPDSEALPA	APALTELGLHNFSEAGLRMLSEGLAWPQ
caspase_recruitment_protein	(844)	LACGGLTADL	CKDLAFGLRAN	TLTDLDSHNVLMQAGAKHLCCQRDQPE
crispypyrin	(775)	LGRGGLSHCC	PLISLVSSNCK	VELELSDNALGFGIRLDCVGLKHL
Nucleotide_Binding_site	(700)	LVSCSANTQ	QWADLSLAEV	NQSLTCVNLSDNELEEGAKDLTTTRHPP
		1001		1050
HLRPS11	(493)	PRVCTV	YVQLPEQ	FGIYLVGMLECSALTTLDISGQCPAPMYTYLC
caspase_recruitment_protein	(894)	CLLQRL	KLVSCELT	SLCCOBLASVLSAPSIKELDLQINNEDEVGVRLIC
crispypyrin	(820)	CNLKKL	KLVSCELT	SACCOBLASVLSTSHSLTFLYVGEMALGDSGVAILC
Nucleotide_Binding_site	(610)	CLLQRL	KLLENCHL	TEANKRLAAVHVVSFELTHLCIAKNPIGNTGVKFLC
		1051		1100
HLRPS11	(543)	AVDCHQGE	ELQTES	ASVELSEQNLOELQVVKRAEDVTHALDGHPO
caspase_recruitment_protein	(944)	EGLRHACH	LIFGLDQT	TLSDENFOELFALEQENFQLIFSEFSPVMV
crispypyrin	(875)	ERAKNPK	ENLQKGLV	NSCITSVCSALSSVLTNQNTHTHYLRGHTLGC
Nucleotide_Binding_site	(862)	EGLYPECK	LQTEVWNC	DITSDECLLTKLQESSLLCDELGLNHIG
		1101		1150
HLRPS11	(593)	PKFELISTF	-----	-----
caspase_recruitment_protein	(994)	PIEGLDTG	EMSNSTSS	LRKRLGLERAASHVAQANLKLDDSFIFPIAEI
crispypyrin	(925)	KQIKLL	CEGLLHPECK	LQVLELNCNLTSHCWDLSTLLTSQSIRKLSL
Nucleotide_Binding_site	(912)	KGMRFCL	BALEFELCN	RLTWLWGCISIPFSCEDLCSALSNQSTVTLDL
		1151		1200
HLRPS11	(643)	AEESSPEV	VPVVELLCVPS	PASQCDLHTKPLGTDDEFWGFTGPVATEVVDK
caspase_recruitment_protein	(1044)	GNN---	DLGDLGVM	MFCEILKQSCLLQNLGLSEMYFETKPSALDTLOE
crispypyrin	(975)	GNN---	PLGSSGV	FMLEFETCSSTLFTFLRLIDFENDELNKLDEIEE
Nucleotide_Binding_site	(961)	GNN---	PLGSSGV	FMLEFETCSSTLFTFLRLIDFENDELNKLDEIEE

Figure 2C

		1201	1250
HLRRII	(626)	-----	-----
caspase_recruitment_protein	(1094)	EENLYRHEEPVAGSYRWPNTGLCEVVREAVTVEIEFCVWDQFLGEINPQH	
eryopyrin	(1022)	EEFEETVFEPSW-----	
Nucleotide_Binding_site	(1008)	KNFQIIDTEKHHFWAERPSSHDEMI-----	
		1251	1300
HLRRII	(626)	-----	-----
caspase_recruitment_protein	(1094)	SWMVAGPLLDIFAEPGAVEAVHLPHFVALQGQHVDTSLFQVAHFKEEGML	
eryopyrin	(1035)	-----	
Nucleotide_Binding_site	(1034)	-----	
		1301	1350
HLRRII	(626)	-----	-----
caspase_recruitment_protein	(1094)	LEKPARVELHHIVLENPSFSPLGVLLKMIHNALRFIPVTSVVLLYHRLHP	
eryopyrin	(1035)	-----	
Nucleotide_Binding_site	(1034)	-----	
		1351	1400
HLRRII	(626)	-----	-----
caspase_recruitment_protein	(1094)	EEVTFHLYLIPSDCSIRKELELCYRSPGEDQLFSEFYVGHGSGIRLQVK	
eryopyrin	(1035)	-----	
Nucleotide_Binding_site	(1034)	-----	
		1401	1450
HLRRII	(626)	-----	-----
caspase_recruitment_protein	(1094)	DKHDETLVWEALVEFGDIMPATTLIPFACIAVPSFLDAPQLLHFVDQYRE	
eryopyrin	(1035)	-----	
Nucleotide_Binding_site	(1034)	-----	
		1451	1500
HLRRII	(626)	-----	-----
caspase_recruitment_protein	(1094)	QLIARVTSVEVVLMELHGVLSQEQYREVLAEENTRFSQMEFLFGLQSWI	
eryopyrin	(1035)	-----	
Nucleotide_Binding_site	(1034)	-----	
		1501	1536
HLRRII	(626)	-----	-----
caspase_recruitment_protein	(1094)	RECKDGLYQALKETHPHLIMELWEKGSKEGGLPLSS	
eryopyrin	(1035)	-----	
Nucleotide_Binding_site	(1034)	-----	

Figure 3

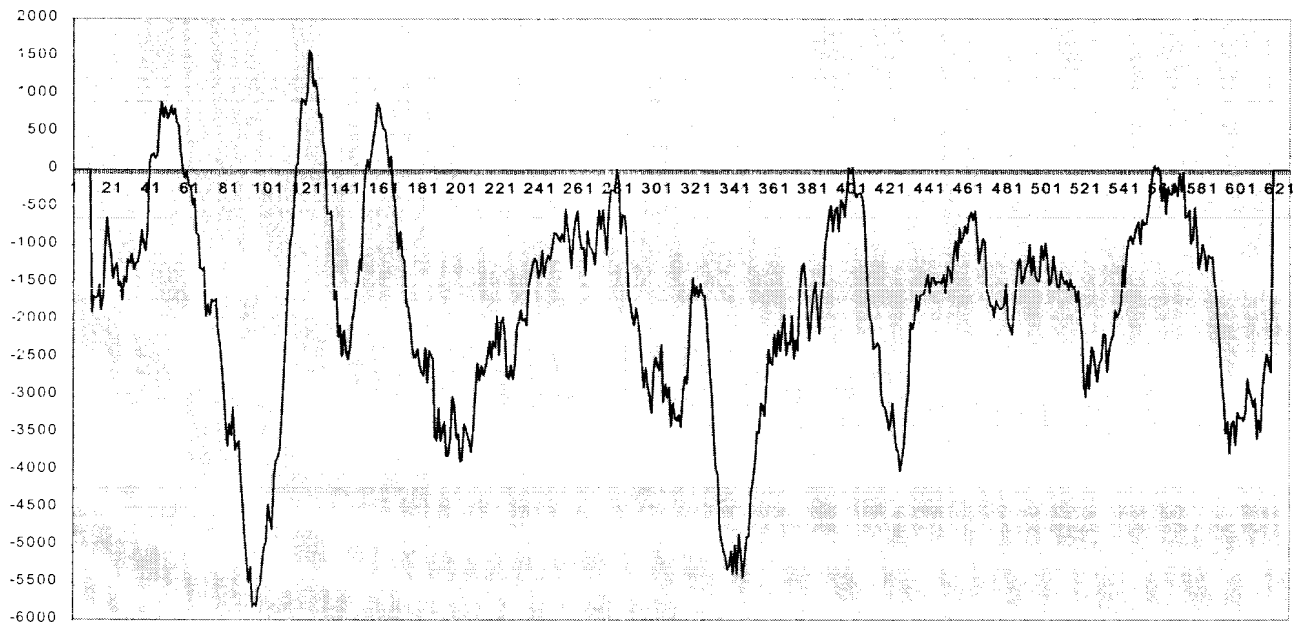


Figure 4

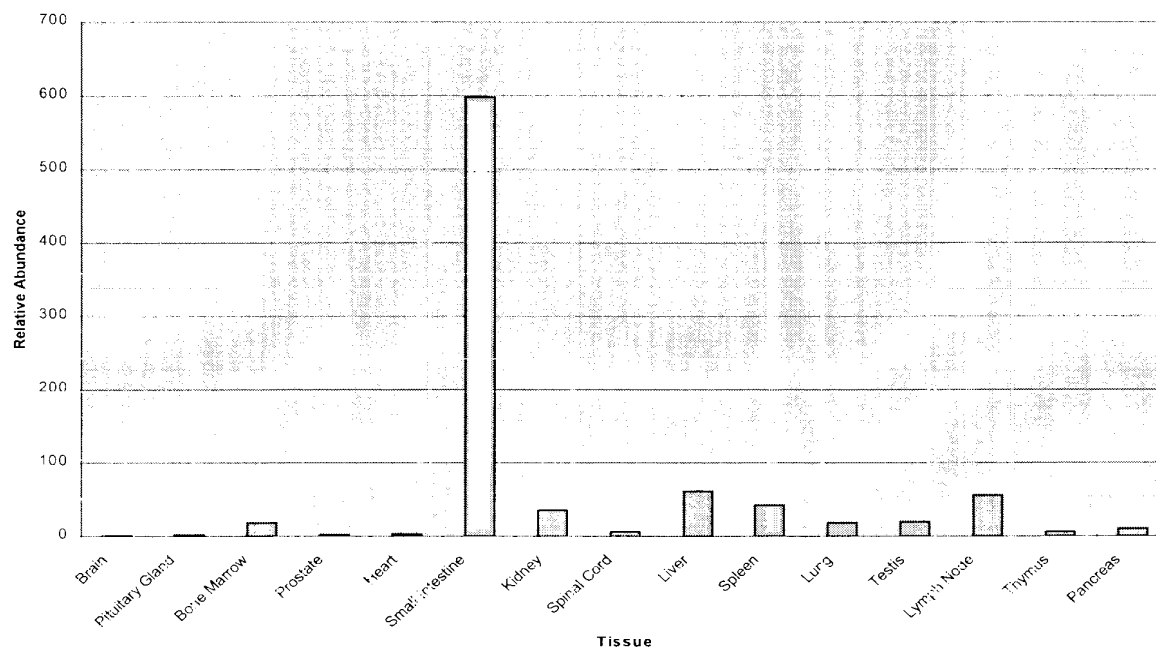


Figure 5.

Protein	Genbank ID	Identities	Similarities
human caspase recruitment protein 7	gi 10198209	36.3%	44.0%
human nucleotide binding site protein	gi 10198207	35.0%	42.2%
human cryopyrin protein	gi 17027237	35.7%	46.0%